SEQUENCE LISTING

<110> Amit, Ido
Yakir , Liat
Yarden, Yosef

<120> POLYNUCLEOTIDES, POLYPEPTIDES AND ANTIBODIES AND USE THEREOF IN TREATING TSG101-ASSOCIATED DISEASES

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Ala Pro Val Glu Gln Met Trp Ser Met Gly Lys Gly Ser Ser Val Gln
            740                 745                 750

Gly Glu Arg Glu Met Val Ser Glu Gln Arg Trp Ala Leu Ser Asn Leu
        755                 760                 765

Leu Gln Gln Leu Leu Lys Glu Lys Lys Gln Arg Glu Glu Glu Leu His
    770                 775                 780

Gly Ile Leu Ala Glu Leu Glu Ala Lys Ser Glu Thr Lys Gln Glu Asn
785                 790                 795                 800

Tyr Trp Leu Ile Gln Tyr Gln Arg Leu Leu Asn Gln Lys Pro Leu Ser
                805                 810                 815

Leu Lys Leu Gln Glu Glu Gly Met Glu Arg Gln Leu Val Ala Leu Leu
            820                 825                 830

Val Glu Leu Ser Ala Glu His Tyr Leu Pro Leu Phe Ala His His Arg
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835 840 845

Ile Thr Leu Asp Met Leu Ser Arg Met Gly Pro Gly Asp Leu Ala Lys
850 855 860

Val Gly Val Ser Glu Ala Gly Leu Gln His Glu Ile Leu Arg Arg Ala
865 870 875 880

Arg Asp Leu Leu Asp Val Ala Arg Val Gln Pro Glu Leu Lys Pro Pro
885 890 895

Lys Asn Glu Val Phe Gly Val Ser Glu Pro Pro Thr Ala Pro Gln Glu
900 905 910

Leu Pro Glu Ser Val Arg Pro Ser Ala Pro Pro Ala Glu Leu Asp Val
915 920 925

Pro Thr Ser Glu Cys Val Val Cys Leu Glu Arg Glu Ala Gln Met Val
930 935 940

Phe Leu Thr Cys Gly His Val Cys Cys Cys Gln Gln Cys Cys Gln Pro
945 950 955 960

Leu Arg Thr Cys Pro Leu Cys Arg Gln Glu Ile Ser Gln Arg Leu Arg
965 970 975

Ile Tyr His Ser Ser
980

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<213> Homo sapiens

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1 5 10 15

Glu Gln Arg Trp Ala Leu Ser Ser Leu Leu Gln Gln Leu Leu Lys Glu
20 25 30

Lys Gln Gln Arg Glu Glu Glu Leu Arg Glu Ile Leu Thr Glu Leu Glu
35 40 45

Ala Lys Ser Glu Thr Arg Gln Glu Asn Tyr Trp Leu Ile Gln Tyr Gln
50 55 60

Arg Leu Leu Asn Gln Lys Pro Leu Ser Leu Lys Leu Gln Glu Glu Gly
65 70 75 80

Met Glu Arg Gln Leu Val Ala Leu Leu Glu Glu Leu Ser Ala Glu His
85 90 95

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Tyr Leu Pro Ile Phe Ala His His Arg Leu Ser Leu Asp Leu Leu Ser
            100                 105                 110

Gln Met Ser Pro Gly Asp Leu Ala Lys Val Gly Val Ser Glu Ala Gly
        115                 120                 125

Leu Gln His Glu Ile Leu Arg Arg Val Gln Glu Leu Leu Asp Ala Ala
    130                 135                 140

Arg Ile Gln Pro Glu Leu Lys Pro Pro Met Gly Glu Val Val Thr Pro
145                 150                 155                 160

Thr Ala Pro Gln Glu Pro Pro Glu Ser Val Arg Pro Ser Ala Pro Pro
                165                 170                 175

Ala Glu Leu Glu Val Gln Ala Ser Glu Cys Val Val Cys Leu Glu Arg
            180                 185                 190

Glu Ala Gln Met Ile Phe Leu Asn Cys Gly His Val Cys Cys Cys Gln
        195                 200                 205

Gln Cys Cys Gln Pro Leu Arg Thr Cys Pro Leu Cys Arg Gln Asp Ile
    210                 215                 220

Ala Gln Arg Leu Arg Ile Tyr His Ser Ser
225                 230
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<213> Homo sapiens

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<400> 8

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Val Thr Pro Thr Ala Pro Gln Glu Pro Pro Glu Ser Val Arg Pro Ser
1               5                   10                  15

Ala Pro Pro Ala Glu Leu Glu Val Gln Ala Ser Glu Cys Val Val Cys
            20                  25                  30

Leu Glu Arg Glu Ala Gln Met Ile Phe Leu Asn Cys Gly His Val Cys
        35                  40                  45

Cys Cys Gln Gln Cys Cys Gln Pro Leu Arg Thr Cys Pro Leu Cys Arg
    50                  55                  60

Gln Asp Ile Ala Gln Arg Leu Arg Ile Tyr His Ser Ser
65                  70                  75
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cctcgagtca gtagaggtca ctgagaccg 29

<210> 11
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<220>
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ggaattcggg cttattcagg tcatgattg 29

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aaactgcagc cagagcagaa ctgagttctt catcc 35

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cctgcagagc tggaggtgc 19

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gacgacctca cccattggtg 20

<210> 17
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gtatgtatta cctctataag gcac 24

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gggcttattc aggtcatgat tgt 23

<210> 19
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cacaatcatg acctgaataa gcc 23

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<210> 22

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cattcccaca gctcccttat ac 22

<210> 23
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gtataaggga gctgtgggaa tg 22

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ggaggtggag actacaagga c 21

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ccgggatcca tggcggtgtc ggag 24

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ctcttcttgc agcttcaagg 20

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gccaggatcc agccagag 18

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cctgcagagc tggaggtgc 19

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gacgacctca cccattggtg 20

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gaggagctgt cggctgagc 19

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Ala Pro Pro

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cctcagctcc ctgctccagc agctgctcaa agagaagcag cagcgagagg aagagctccg 120

ggaaatcctg acggagttag aagccaaaag tgaaaccagg caggaaaatt actggctgat 180

tcagtatcaa cggcttttga accagaagcc cttgtccttg aagctgcaag aagaggggat 240

ggagcgccag ctggtggccc tcctggagga gctgtcggct gagcactacc tgcccatctt 300

tgcgcaccac cgcctctcac tggacctgct gagccaaatg agcccagggg acctggccaa 360

ggtgggcgtc tcagaagctg gcctgcagca cgagatcctc cggagagtcc aggaactgct 420

ggatgcagcc aggatccagc cagagctgaa accaccaatg ggtgaggtcg tcacccctac 480

ggcccccccag gagcctcctg agtctgtgag gccatccgct ccccctgcag agctggaggt 540

gcaggcctca gagtgtgtcg tgtgcctgga acgggaggcc cagatgatct tcctcaactg 600

tggccacgtc tgctgctgcc agcagtgctg ccagccactg cgcacctgcc cgctgtgccg 660

ccaggacatc gcccagcgcc tccgcatcta ccacagcagc 700

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gagctggagg tgcaggcctc agagtgtgtc gtgtgcctgg aacgggaggc ccagatgatc 120

ttcctcaact gtggccacgt ctgctgctgc cagcagtgct gccagccact gcgcacctgc 180

ccgctgtgcc gccaggacat cgcccagcgc ctccgcatct accacagcag c 231

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ttggagguca gaagagagca g 21

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guccaaaggu uccggagact t 21

<210> 44
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ttcagguuuc caaggccucu g 21

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Glu Val Val Thr Pro Thr Ala Pro Gln Glu Pro Pro Glu Ser Val Arg
1 5 10 15

Pro Ser Ala Pro Pro Ala Glu
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aagaattcag aggtcgtcac ccctacgg 28

<210> 53
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aaggatccct ctgcaggggg agcgg 25